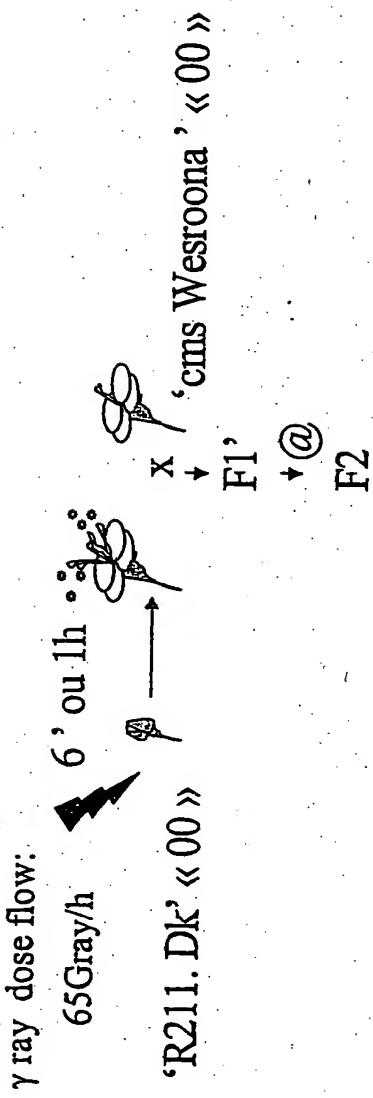


Fig 1



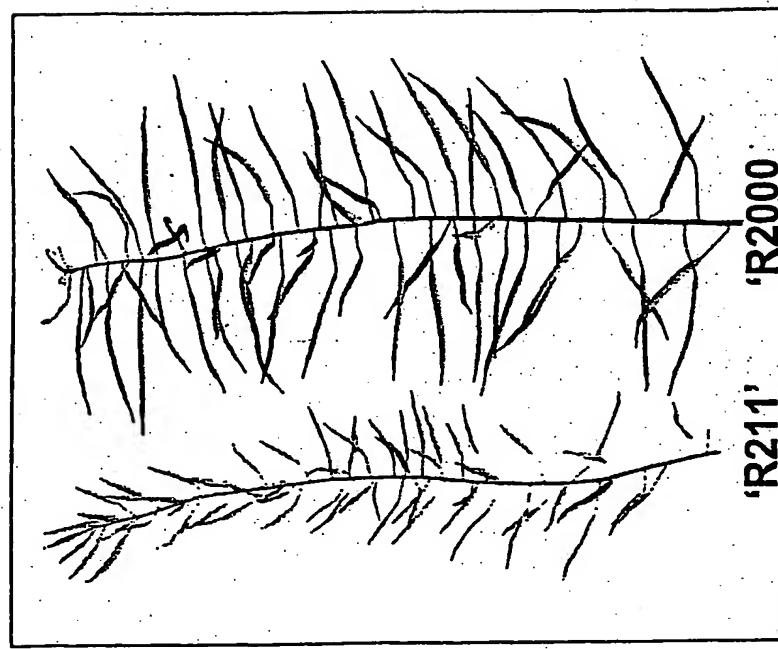


Fig. 1: Seed set on 'R211' and 'R2000'

Fig 2

Fig 3

Genotype	Selfings	Test Crosses
Drakkar	29.3	
Pactol	23.1	
R211	11.2	25.5
R2000	26.5 (24.0 – 31.1)	27.0 (24.0 – 28.7)

Fig 4

Fig 5

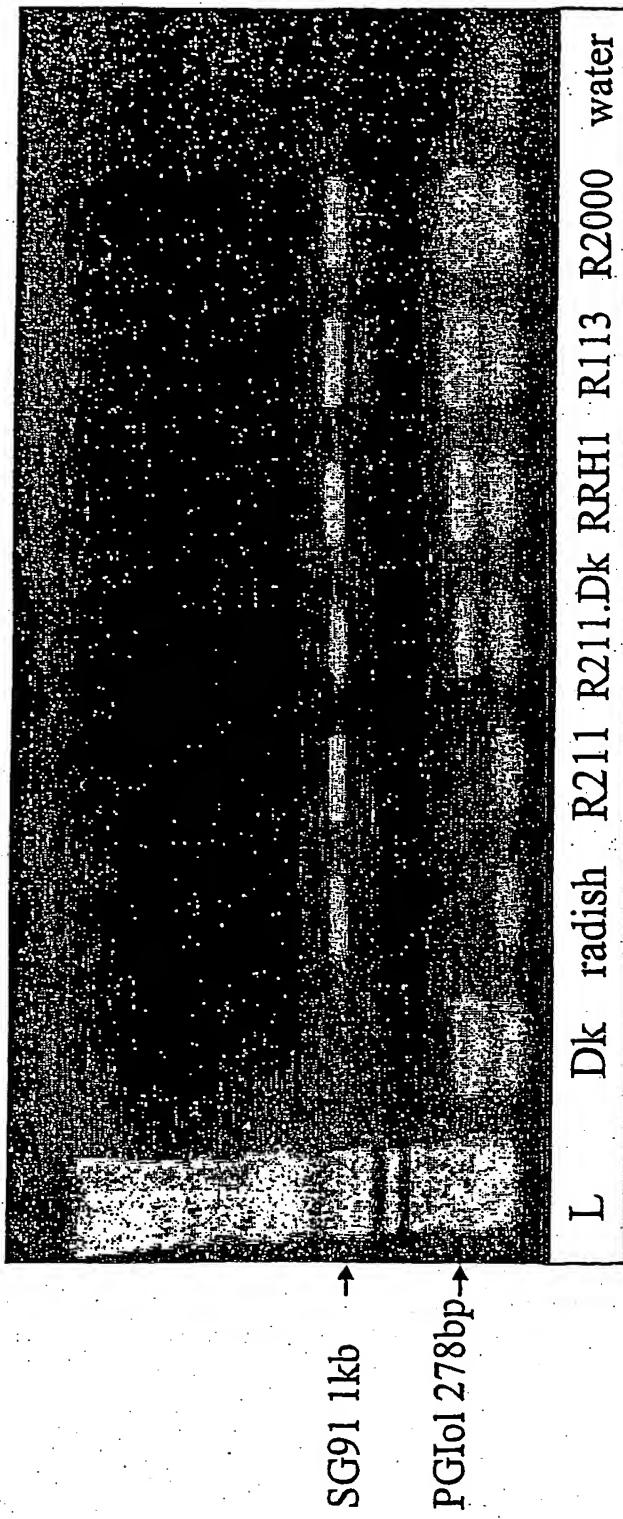
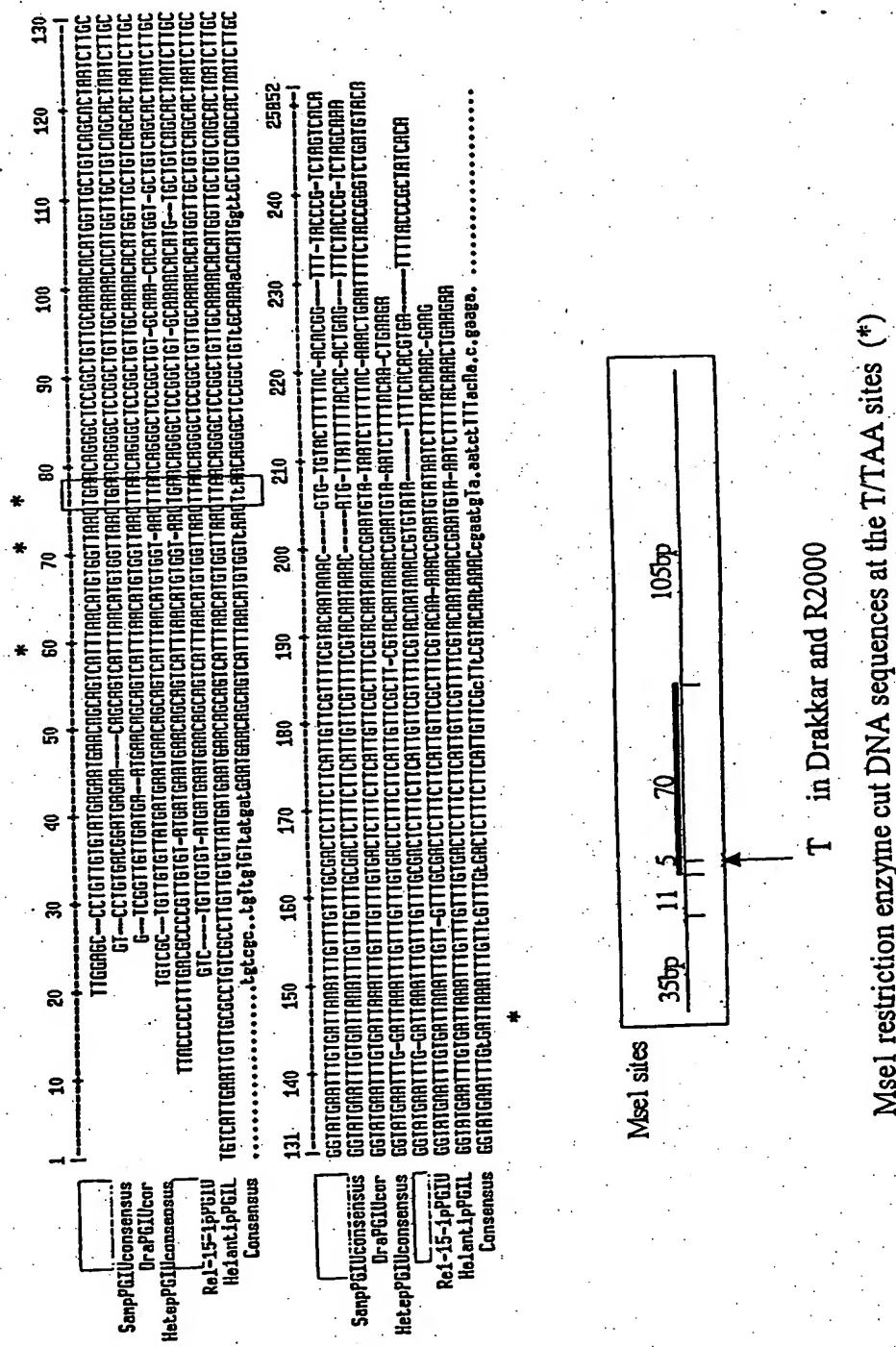


Fig 6



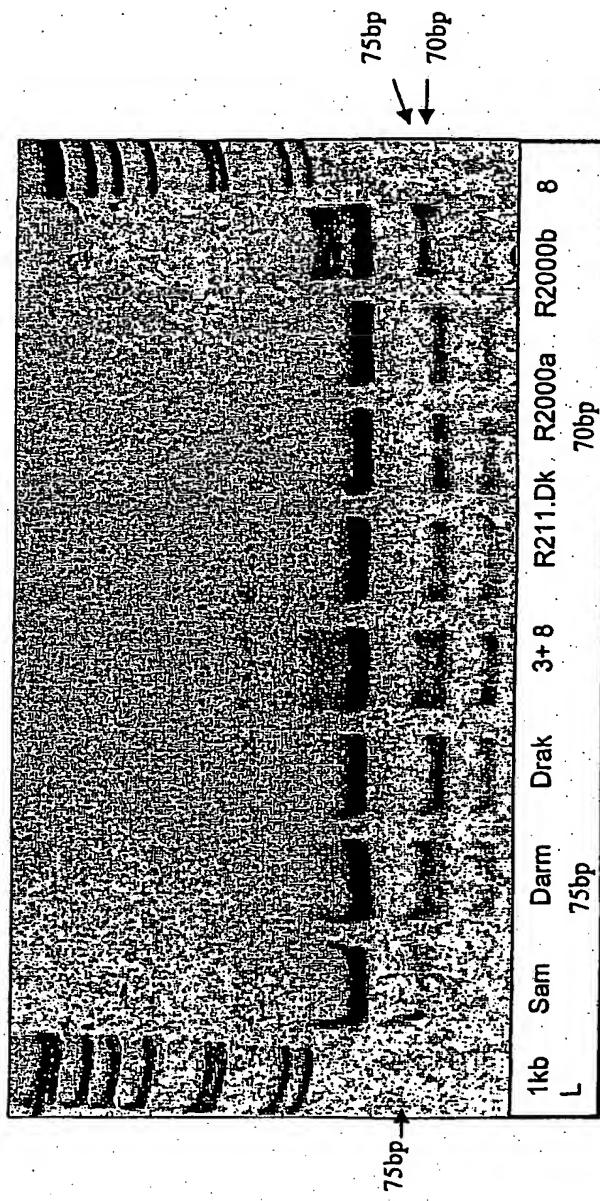


Fig 7

Fig 8

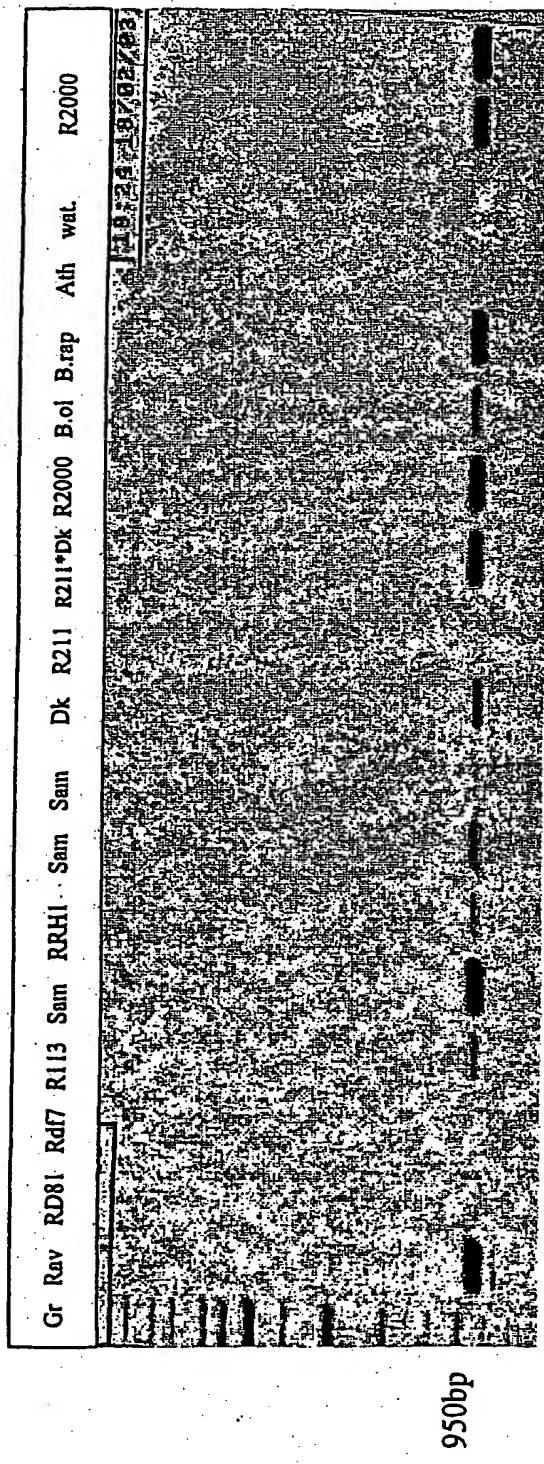


Fig 9

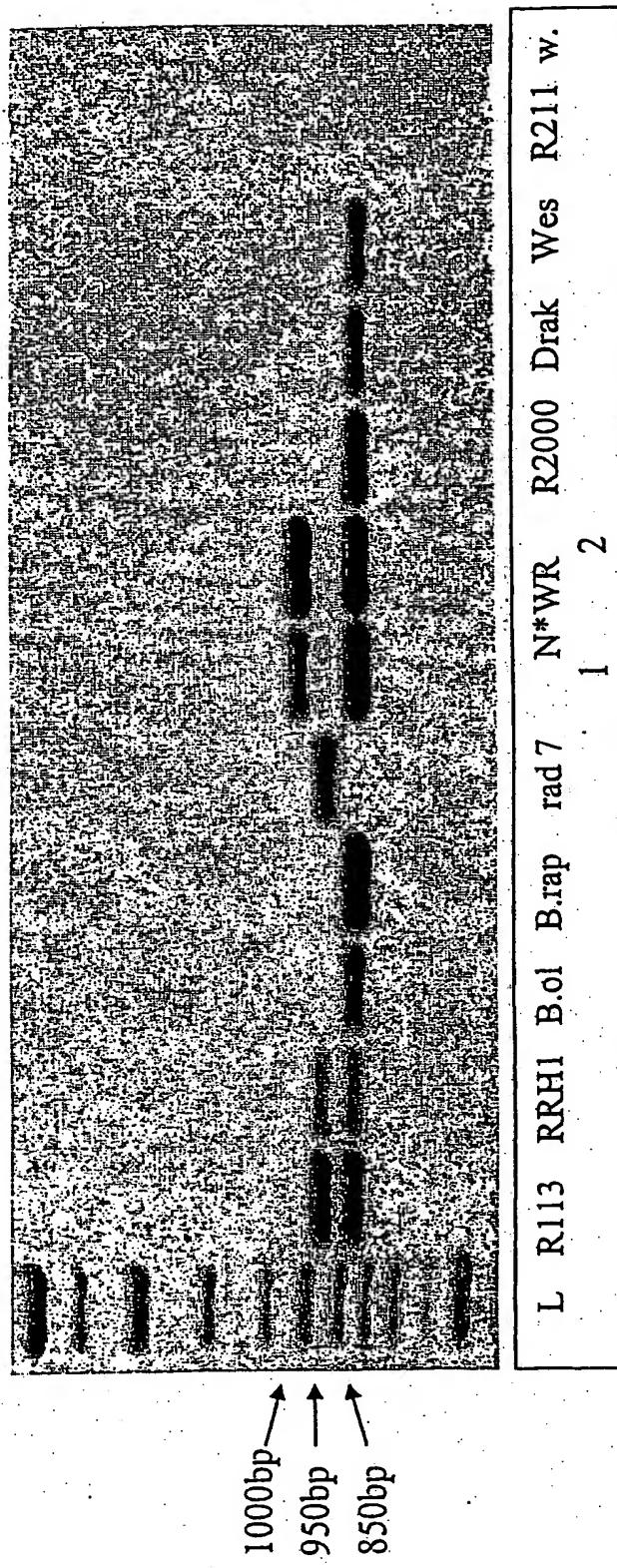
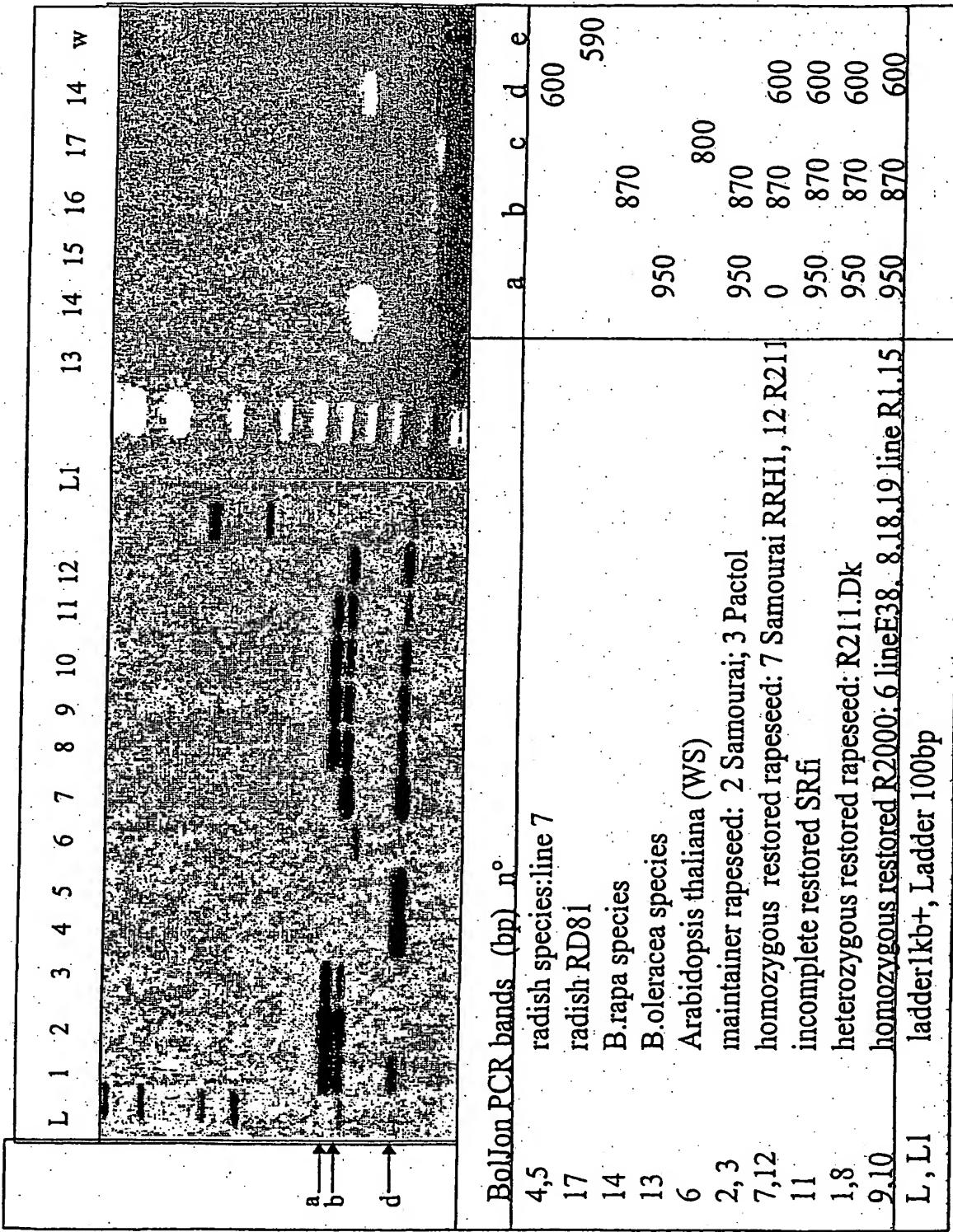


Fig 10



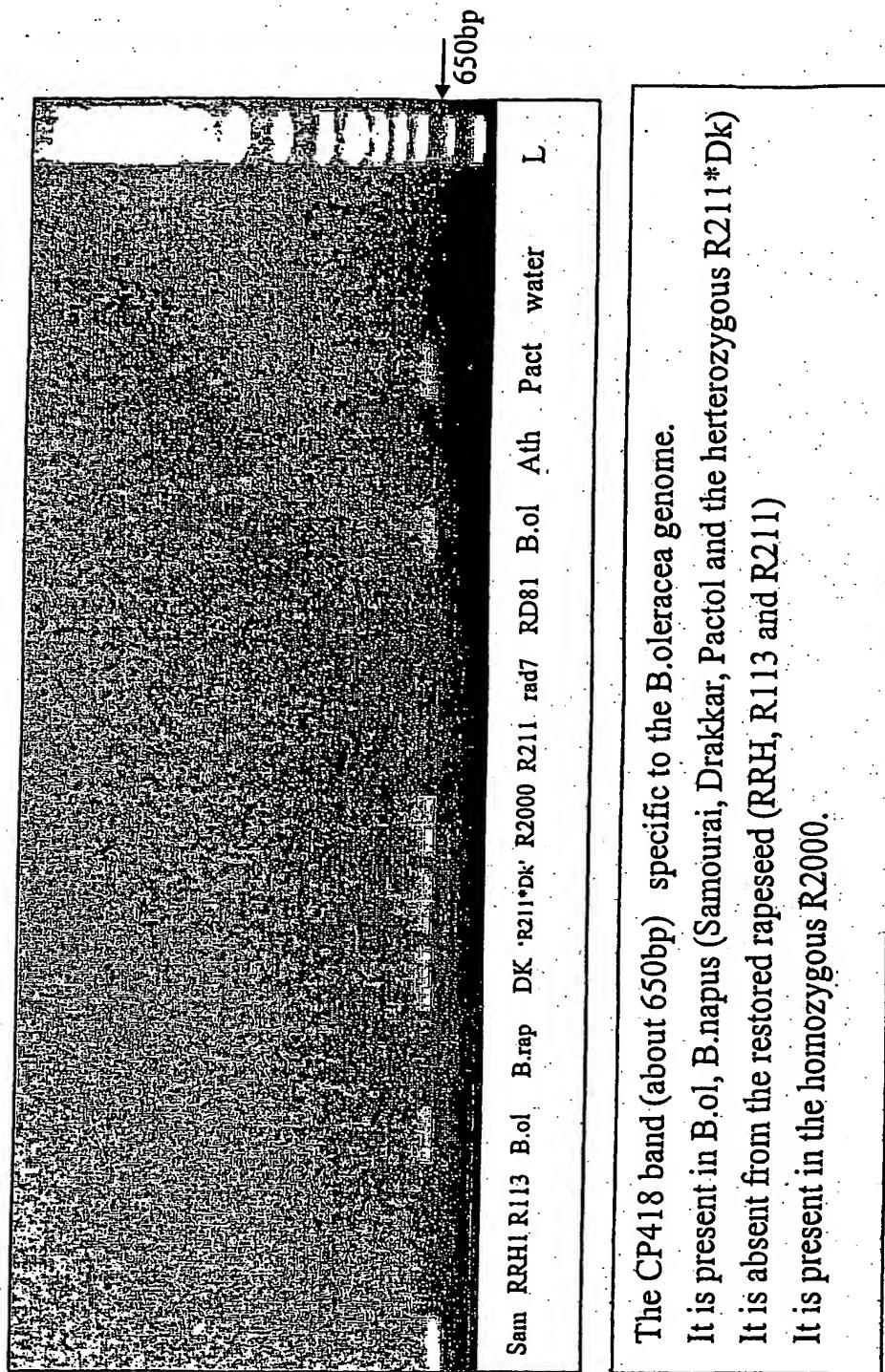


Fig 11

Figure 12

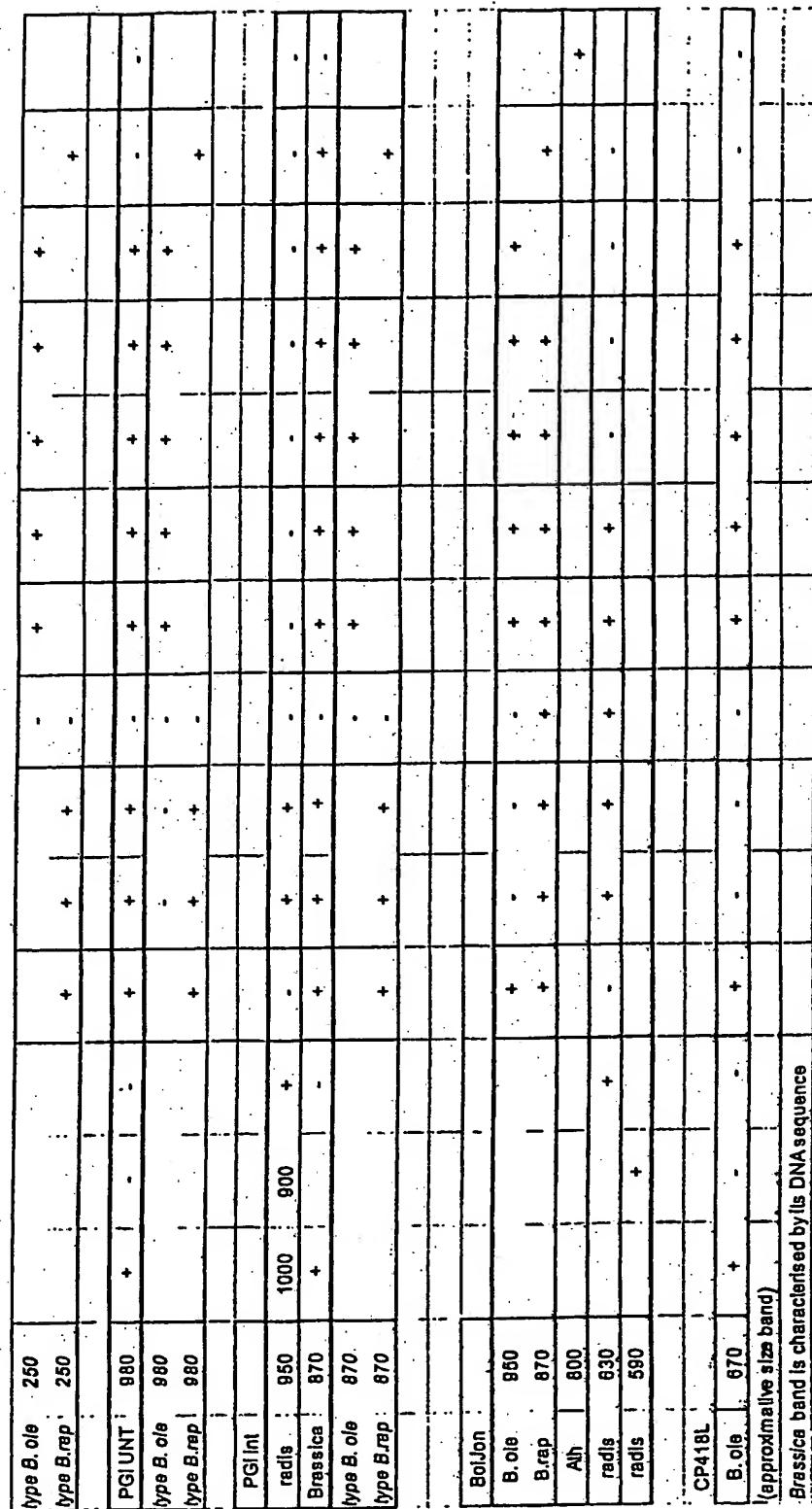


Figure 13 (a)

51 81 PGIol U --> 100

consePGIintTUNDrakka
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera
consePGIintUNTR2000
Consensus

TTGCTTAGCG TCCAAATTC ATGATTGTAT TCATTTGATT GTTGTG
TTGCTTAGCG TCCAAATTC ATGATTGTAT TCATTTGATT GTTGTGTGAC
TTG... TCATT.GA... TTGT.TGCG

1

101 150

consePGIintTUNDrakka
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera
consePGIintUNTR2000
Consensus

GTCG TTTGTTGGTG AGT.GAACAG CAGTCATTTA
GCCTGTTG TGTATGATG AAT.GAACAG CAGTCATTTA
GCCCGGTTG G TAT.GAACAG CAG.CATTTA
..... G CAGTCATTTA
..... CG TGTGAGAAG CAG.CATTTA
CCTG TCGCCTTGTG TGTATGATG AAT.GAACAG CAGTCATTTA
TATCGCCTC. TCGCCTTGTG TGTATGATG AAT.GAACAG CAGTCATTTA
CCTG TCGCCTTGTG TGTATGATG AAT.GAACAG CAGTCATTTA
..... t.g g ... t.gaa.ag cagtcattta

151 200

consePGIintTUNDrakka
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera
consePGIintUNTR2000
Consensus

ACATG.TGGT TAACTAAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
ACATG.TGGT TAACTAAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
ACATG.TGGT .AACTGAACA GGGCTCCGGC TGTTGCCCC.. CTAAGGGTTG
ACATGGTGGT TAACTGAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
ACATG..GGT ..ACTGAACA GGGC.CCGGC TGTTGCAA.. ACAG...TG
ACATG.TGGT TAACTAAACA GGGCTCAGGC TGTTGCAAAA CACATGGTTG
ACATG.TGGT TAACTAAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
ACATG.TGGT TAACTAAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
ACATG.TGGT TAACTAAACA GGGCTCCGGC TGTTGCAAAA CACATGGTTG
acatg.tggtaactaaaca gggctccggc tgttgcaaaa cacatggttg

2

250

consePGIintTUNDrakka
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera
consePGIintUNTR2000
Consensus

CTGT PGI int U -->
CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTGTT
CTGT CAGCAC TAATCTTGC GGTATG AATT TGTGATTAAA TTTGTTGTT
ctgtcagcac taatcttgc ggtatg aatt tgtgattaaa tttgttgt

300

consePGIintTUNDrakka
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera
consePGIintUNTR2000
Consensus

TGTGACTCTT T.CTTCATTG TTCTGTTTCG TACAATAAAC CGAATGTATA
TGTGACTCTT T.CTTCATTG TTCTGTTTCG TACAATAAAC CGAATGTATA
TGCAGCTCTT T.CTTCATTG TTCTGTTTCG TACAATAAAC ..AATGTATA
TGCAGCTCTT T.CTTCATTG TTCTGTTTCG TACAATAAAC ..AATGTATA
TGCAGCTCTT T.CTTCATTG TTCTGTTTCG TACAATAAAC ..AATGTATA
TGTGACTCTT T.CTTCATTG TTCTGTTTCG TACAATAAAC CGAATGTATA
TGTGACTCTT TTCTCATTG TTCTGTTTCG TACAATAAAC CGAATGTATA
TG.GACTCTT T.CTTCATTG TTCTGTTTCG TACAATAAAC CGAATGTATA
TGTGACTCTT T.CTTCATTG TTCTGTTTCG TACAATAAAC CGAATGTATA
tg.gactctt t.cttcattg ttctgtttcg tacaataaac CGAATGTATA
13

Figure 13 (b)

	301	<--- PGIol antL 341	350
consePGIintTUNTDrakka	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consensWesrPGI	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR113	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBrapaA	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
ConsePGIintUNTRRH1	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBo-EM:AF258277	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBra-EM:AF258278	ACCTTTTAC AAACTGAA	AT GTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBolera	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR2000	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
Consensus	atcttttac aaactgaa	tt ttctacccggg tctgatgtac a	atgctAGTC

Figure 14 (a)

201	PGI int U --->	250	
consePGIintTUNDRAKKA	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
consensWesrPGI	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
consePGIintUNTR113	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
consePGIintUNTBRAPA	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
ConsePGIintUNTRRH1	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
PGIBo-EM:AF258277	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
PGIBra-EM:AF258278	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
consePGIintUNTbolera	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
consePGIintUNTR2000	CTGT CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGT	
Consensus	ctgtcagcac taatcttgc ggtatg	aatt tgtgattaaa ttgtttgt	
251		300	
consePGIintTUNDRAKKA	TGTGACTCTT T. CTTCATTG TTCGTTTCG TACAATAAAC	CGAATGTATA	
consensWesrPGI	TGTGACTCTT T. CTTCATTG TTCGTTTCG TACAATAAAC	CGAATGTATA	
consePGIintUNTR113	TGCGACTCTT T. CTTCATTG TTCGTTTCG TACAATAAAC	AAATGTATA	
consePGIintUNTBRAPA	TGCGACTCTT T. CTTCATTG TTCGTTTCG TACAATAAAC	AAATGTATA	
ConsePGIintUNTRRH1	TGCGACTCTT T. CTTCATTG TTCGTTTCG TACAATAAAC	AAATGTATA	
PGIBo-EM:AF258277	TGCGACTCTT T. CTTCATTG TTCGTTTCG TACAATAAAC	AAATGTATA	
PGIBra-EM:AF258278	TGCGACTCTT TTCTTCATTG TTCGTTTCG TACAATAAAC	CGAATGTATA	
consePGIintUNTbolera	TG.GACTCTT T. CTTCATTG TTCGTTTCG TACAATAAAC	CGAATGTATA	
consePGIintUNTR2000	TGCGACTCTT T. CTTCATTG TTCGTTTCG TACAATAAAC	CGAATGTATA	
Consensus	tg.gactctt t_cttcattg ttgcgtttcg tacaataaac	cgaaatgtata	
		e3	
301	<---	PGIol antL 341	350
consePGIintTUNDRAKKA	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consensWesrPGI	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR113	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBRAPA	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
ConsePGIintUNTRRH1	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBo-EM:AF258277	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBra-EM:AF258278	ACCTTTTAC AAACTGAA	AT GTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTbolera	ATCTTTTAC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR2000	ATCTTTT.AC AAACTGAA	TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
Consensus	atcttttac aaactgaa	tt ttctacccggg tctgatgtac a atgctAGTC	
	e		
351			400
consePGIintTUNDRAKKA	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGACAGTA	
consensWesrPGI	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGACAGTA	
consePGIintUNTR113	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGCCAGTA	
consePGIintUNTBRAPA	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGCCAGTA	
ConsePGIintUNTRRH1	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGCCAGTA	
PGIBo-EM:AF258277	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGACAGTA	
PGIBra-EM:AF258278	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGACAGTA	
consePGIintUNTbolera	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGACAGTA	
consePGIintUNTR2000	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGACAGTA	
Consensus	TCCATGTTCT TGGGGATCAT GATTATTTT CTACATGT	TCAGACAGTA	
		e5	e6
401			450
consePGIintTUNDRAKKA	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
consensWesrPGI	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
consePGIintUNTR113	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
consePGIintUNTBRAPA	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
ConsePGIintUNTRRH1	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
PGIBo-EM:AF258277	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
PGIBra-EM:AF258278	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
consePGIintUNTbolera	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
consePGIintUNTR2000	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
Consensus	CAGAAGAAAG TGTT AAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG	
	e7	e	

Figure 14 (b)

consePGIintTUNDrakka	451	end of Data Base PGI sequences	500
consensWesrPGI	AAGTCGGCA	TTGATCCGAA CAATGCATT GCATTTGGG ACTGGGTTGG	
consePGIintUNTR113	AAGTCGGCA	TTGATCCGAA CAATGCATT GCATTTGGG ACTGGGTTGG	
consePGIintUNTBrapaA	AAGTCGGCA	TTGATCCGAA CAATGCATT GCATTTGGG ACTGGGTTGG	
ConsePGIintUNTRRH1	AAGTCGGCA	TTGATCCGAA CAATGCATT GCATTTGGG ACTGGGTTGG	
PGIBo-EM:AF258277	AAGTCGGCA	TTGATCCGAA CAATGCATT GCATTTGGG ACTGGGTTGG	
PGIBra-EM:AF258278	AAGTCGGCA	TTGATCCGAA CAATGCATT GCATTTGGG ACTGGGTTGG	
consePGIintUNTBoleta	AAGTCGGCA	TTGATCCGAA CAATGCATT GCATTTGGG ACTGGGTTGG	
consePGIintUNTR2000	AAGTCGGCA	TTGATCCGAA CAATGCATT GCATTTGGG ACTGGGTTGG	
Consensus	AAGTCGGCA	TTGATCCGAA caatgcatt gcattttggg actgggttgg	
consePGIintTUNDrakka	501		550
consensWesrPGI	TGGAAGGTAC	AGTGGTAAGT GCTTGTAT TTGGTTGTAT AAATTCTCG	
consePGIintUNTR113	TGGAAGGTAC	AGTGGTAAGT GCTTGTAT TTGGTTGTAT AAATTCTCG	
consePGIintUNTBrapaA	TGGAAGGTAC	AGTGGTAAGT GCTTGTAT TTGGTTGTAT TAATTCTCA	
ConsePGIintUNTRRH1	TGGAAGGTAC	AGTGGTAAGT GCTTGTAT TTGGTTGTAT TAATTCTCA	
PGIBo-EM:AF258277	TGGAAGGTAC	AGTGGTAAGT GCTTGTAT TTGGTTGTAT TAATTCTCA	
PGIBra-EM:AF258278	TGGAAGGTAC	AGTGGTAAGT GCTTGTAT TTGGTTGTAT TAATTCTCA	
consePGIintUNTBoleta	TGGAAGGTAC	AGTGGTAAGT GCTTGTAT TTGGTTGTAT AAATTCTCG	
consePGIintUNTR2000	TGGAAGGTAC	AGTGGTAAGT GCTTGTAT TTGGTTGTAT AAATTCTCG	
Consensus	tggaaaggta	actggtaagt gcttgttat ttgggtgtat aaattctcg	
consePGIintTUNDrakka	551		600
consensWesrPGI	TCCATATCCG	CTTGCTTAGT GTATAACTGA AATTCTTTG CAGTTGCAG	
consePGIintUNTR113	TCCATATCCG	CTTGCTTAGT GTATAACTGA AATTCTTTG CAGTTGCAG	
consePGIintUNTBrapaA	TCCATATCCG	CTTGCTTAGT TTATAACTGA AATTCTTTG CAGTTGCAG	
ConsePGIintUNTRRH1	TCCATATCCG	CTTGCTTAGT TTATAACTGA AATTCTTTG CAGTTGCAG	
PGIBo-EM:AF258277	TCCATATCCG	CTTGCTTAGT TTATAACTGA AATTCTTTG CAGTTGCAG	
PGIBra-EM:AF258278	TCCATATCCG	CTTGCTTAGT TTATAACTGA AATTCTTTG CAGTTGCAG	
consePGIintUNTBoleta	TCCATATCCG	CTTGCTTAGT GTATAACTGA AATTCTTTG CAGTTGCAG	
consePGIintUNTR2000	TCCATATCCG	CTTGCTTAGT GTATAACTGA AATTCTTTG CAGTTGCAG	
Consensus	tccatatccg	cttgcttagt ttataactga aattctttg cagttgcag	
consePGIintTUNDrakka	601		650
consensWesrPGI	TGCTGTTGGA	GTCTTACCAT TGTCTCTACA GTATGGCTTC TGTGTTGG	
consePGIintUNTR113	TGCTGTTGGA	GTCTTACCAT TGTCTCTACA GTATGGCTTC TGTGTTGG	
consePGIintUNTBrapaA	TGCTGTTGGA	GTCTTACCAT TGTCTCTACA GTATGGCTTC TCGTGGTTG	
ConsePGIintUNTRRH1	TGCTGTTGGA	GTCTTACCAT TGTCTCTACA GTATGGCTTC TCGTGGTTG	
PGIBo-EM:AF258277	TGCTGTTGGA	GTCTTACCAT TGTCTCTACA GTATGGCTTC TCGTGGTTG	
PGIBra-EM:AF258278	TGCTGTTGGA	GTCTTACCAT TGTCTCTACA GTATGGCTTC TCGTGGTTG	
consePGIintUNTBoleta	TGCTGTTGGA	GTCTTACCAT TGTCTCTACA GTATGGCTTC TCGTGGTTG	
consePGIintUNTR2000	TGCTGTTGGA	GTCTTACCAT TGTCTCTACA GTATGGCTTC TCGTGGTTG	
Consensus	tgctgttgg	gtcttaccat tgtctctaca gtatggcttc tcgtggttg	
consePGIintTUNDrakka	651		700
consensWesrPGI	AGAAAGTACGG	TACCTTCTAC TTTATAGCC ATCTCATAAA ATGTCTTGG	
consePGIintUNTR113	AGAAAGTACGG	TACCTTCTAC TTTATAGCC ATCTCATAAA ATGTCTTGG	
consePGIintUNTBrapaA	AGAAAGTACGG	TACCTTCTAC TTTATAGCC ATCTCATAAA ATGTCTTGG	
ConsePGIintUNTRRH1	AGAAAGTACGG	TACCTTCTAC TTTATAGCC ATCTCATAAA ATGTCTTGG	
PGIBo-EM:AF258277	AGAAAGTACGG	TACCTTCTAC TTTATAGCC ATCTCATAAA ATGTCTTGG	
PGIBra-EM:AF258278	AGAAAGTACGG	TACCTTCTAC TTTATAGCC ATCTCATAAA ATGTCTTGG	
consePGIintUNTBoleta	AGAAAGTACGG	TACCTTCTAC TTTATAGCC ATCTCATAAA ATGTCTTGG	
consePGIintUNTR2000	AGAAAGTACGG	TACCTTCTAC TTTATAGCC ATCTCATAAA ATGTCTTGG	
Consensus	agaagtacgg	taccttctac tttatagcc atctcataaa atgtcttgg	

Figure 14 (c)

701 750

consePGIintTUNDrakka
 consensWesrPGI
 consePGIintUNTR113
 consePGIintUNTBrapaA
 ConsePGIintUNTRRH1
 PGIBo-EM:AF258277
 PGIBra-EM:AF258278
 consePGIintUNT Bolera
 consePGIintUNTR2000
 Consensus

CATATTCTTT CTATTTTATT TTCCCTCTTAA TGATTTCTTC TTTTTTTTAT
 CATATTCTTT CTATTTTATT TTCCCTCTTAA TGATTTCTTC TTTTTTTTAT
 CATATTCTTT CTATTTTATT TTCCCTCTGAA TGATTTCTTC TCTTTTAT..
 CATATTCTTT CTATTTTATT TTCCCTCTGAA TGATTTCTTC TCTTTTAT..
 CATATTCTTT CTATTTTATT TTCCCTCTGAA TGATTTCTTC TCTTTTAT..

 CATATTCTTT CTATTTTATT TTCCCTCTTAA TGATTTCTTC TTTTTTTA..
 CATATTCTTT CTATTTTATT TTCCCTCTTAA TGATTTCTTC TTTTTTTAT
 catattcttt ctatttatt ttccctcttAA tgatttcttc tttttttt..

15 16 17 800

751
 consePGIintTUNDrakka
 consensWesrPGI
 consePGIintUNTR113
 consePGIintUNTBrapaA
 ConsePGIintUNTRRH1
 PGIBo-EM:AF258277
 PGIBra-EM:AF258278
 consePGIintUNT Bolera
 consePGIintUNTR2000
 Consensus

TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG
 TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG
 TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG
 TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG
 TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG

 TGCATTCCCG TTTTATTTTC AAAAGTTGTC CGGCCCCCTA AACCAAGAAG
 TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG
 tgattcccg ttttattttc aaaagtgt. actgtctcta aatcaagaag

801 850

consePGIintTUNDrakka
 consensWesrPGI
 consePGIintUNTR113
 consePGIintUNTBrapaA
 ConsePGIintUNTRRH1
 PGIBo-EM:AF258277
 PGIBra-EM:AF258278
 consePGIintUNT Bolera
 consePGIintUNTR2000
 Consensus

AAACCTTCTT AGTAGATCCA GGTGATATTG AGCCTTTTTT AAATTGGACT
 AAACCTTCTT AGTAGATCCA GGTGATATTG AGCCTTTTTT AAATTGGACT
 AAACCTTCTT AGTAGATCCA GTGATATTG AGCCTTTCT AAATTGGACT
 AAACCTTCTT AGTAGATCCA G.TGATATTG AGCCTTTCT AAATTGGACT
 AAACCTTCTT AGTAGATCCA GTGATATTG AGCCTTTCT AAATTGGACT

 AAACCTTCTT AGGA...CCA GA...CTCC ACCCTTTTTT AAATTGGACT
 AAACCTTCTT AGTAGATCCA GGTGATATTG AGCCTTTTTT AAATTGGACT
 aaaccttctt agtagatcca g.tgatattg agcctttt.t aaattggact

18 19

851 900

consePGIintTUNDrakka
 consensWesrPGI
 consePGIintUNTR113
 consePGIintUNTBrapaA
 ConsePGIintUNTRRH1
 PGIBo-EM:AF258277
 PGIBra-EM:AF258278
 consePGIintUNT Bolera
 consePGIintUNTR2000
 Consensus

GCAGGGTTTT AAA.GGGAGC TTCAAGCATT GATAGCATT TCCAGTCCCC
 GCAGGGTTTT AAA.GGGAGC TTCAAGCATT GATAGCATT TCCAGTCCAC
 GCAGGGTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..
 GCAGGGTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..
 GCAGGGTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCCAC

 GCAGGGTTTT AAA.GGGGGC TTCAAGCATT GATAGCATT TCCAGTCCAC
 GCAGGGTTTT AAACGGGAGC TTCAAGCATT GATAGCATT TCCAGTCCAC
 gcaggttttt aaa. gggagc ttcaagcatt gatagcatt tccagtcc.c

20

901 950

consePGIintTUNDrakka
 consensWesrPGI
 consePGIintUNTR113
 consePGIintUNTBrapaA
 ConsePGIintUNTRRH1
 PGIBo-EM:AF258277
 PGIBra-EM:AF258278
 consePGIintUNT Bolera
 consePGIintUNTR2000
 Consensus

ACC.GTTTGGA GAAGAAATAA CCCGTGAGTT GCATTAGTT GTGTGATTAT
 ACC.GTTTGGA GAAGAAATAA CCCGTGAGTT GCATTAGTT GTGTGATTAT
 .CCCGTTGGA GAAGAAATAA CCCGTGAGTT GCATTAGTT.. GTGTGATTAT
 .CCCGTTGGA GAAGAAATAA CCCGTGAGTT GCATTAGTT GTGTGATTAT
 ACC.GTTTGGA GAAGAAATAA CCCGTGAGTT GCATTAGTT GTGTGATTAT

 ACCCGTTGGA GAAGAAATAA CCCGTGAGTT GCATTAGTT GTGTGATTAT
 ACC.GTTTGGA GAAGAAATAA CCCGTGAGTT GCATTAGTT GTGTGATTAT
 acc.gtttgaa gaagaataata cccgtgagtt gcattagtt. gtgtgattat

Figure 14 (d)

951	1000
consePGIintTUNDrakka	ACAGTTTTTC TTGTCTTTT GCTATGCCCA TCAACACTAG AAGATTCTGTG
consensWesrPGI	ACAGTTTT.C TTGTCTTTT. GCTATGTCCA TCAACACTAG A.GATTCTGTG
consePGIintUNTR113	ACAGTTTT.C TTGCCTTTT GCTAT..AGG GCAAC.CTAG A.GATTCTGTG
consePGIintUNTBrapaA	ACAGTTTT.C TTGTCTTTT. GCTATG.TCA TCAAC.CTAG A.GATTCTGTG
ConsePGIintUNTRRH1	ACAGTTTT.C TTGTCTTTT GCTAT...AT GCAACCCTAG ..GATTCTGTG
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera	ACAGTTTT.C TTGTCTTTT GCTAG..TGA TCAAC.CTAG A.GATTCTGTG
consePGIintUNTR2000	ACAGTTTT.C TTGTCTTTT GCTATGTCCA TCAACACTAG A.GATTCTGTG
Consensus	acagtttt.c ttgtctttt gctat....a tcaac.ctag a.gattc.tg
	21
1001	1050
consePGIintTUNDrakka	AAGTTATTAG TGTAGCCAAC GCCTAGGGGG AGGTTGGTTG GCTGTTTGG
consensWesrPGI	AAGTTATTAG TGTAGTCAAC GCA.....
consePGIintUNTR113	AAGTTATTAG TGTAGTCAAC GCAGAGGAGA G..TTCACTG ACGG.....
consePGIintUNTBrapaA	AAGTTATTAG TGTAGTCAAC GCAGAGTGAG AGG.TGATTG ..
ConsePGIintUNTRRH1	AAGTTATTAG TGTAGTCAAC GCAGAGGAGG AGATGGTT.....
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera	AAGTTATTAG TGTAGTCAAC GCATAGGAGG AGC.....
consePGIintUNTR2000	AAGTTATTAG TGTAGTCAAC GCATAGGGAG AGGTGAT..GG TGACTTTGG
Consensus	aagttattag tgtagtcaac gca.agg.g..g.....
1051	1076
consePGIintTUNDrakka	ACGTTTCAC GTGCTCCGGG GGGTTTTGG GGACCAAACC CCCAAC
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera
consePGIintUNTR2000	ACGATTTCAG GTGCTTTAGG GTTATTG.....

Figure 15 (a)

EMBH44836anti	51	100
GCP18-5CP418L-Sams
GCP18-2CP418L-Wes
GCP18-4CP418L-R2000
conse129bal-Drak
GCPS18-129Sam-ba2
GCP18-3129R211-ba2
GCP18-10129R20-ba2
Consensus
EMBH44836anti	101	150
GCP18-5CP418L-Sams
GCP18-2CP418L-Wes
GCP18-4CP418L-R2000
conse129bal-Drak
GCPS18-129Sam-ba2
GCP18-3129R211-ba2
GCP18-10129R20-ba2
Consensus
EMBH44836anti	151	200
GCP18-5CP418L-Sams
GCP18-2CP418L-Wes
GCP18-4CP418L-R2000
conse129bal-Drak
GCPS18-129Sam-ba2
GCP18-3129R211-ba2
GCP18-10129R20-ba2
Consensus
EMBH44836anti	201	250
GCP18-5CP418L-Sams
GCP18-2CP418L-Wes
GCP18-4CP418L-R2000
conse129bal-Drak
GCPS18-129Sam-ba2
GCP18-3129R211-ba2
GCP18-10129R20-ba2
Consensus
EMBH44836anti	251	300
GCP18-5CP418L-Sams
GCP18-2CP418L-Wes
GCP18-4CP418L-R2000
conse129bal-Drak
GCPS18-129Sam-ba2
GCP18-3129R211-ba2
GCP18-10129R20-ba2
Consensus
EMBH44836anti	301	350
GCP18-5CP418L-Sams	A. TTGTTT ATACAAAGTT TCACT AAAT CTACAAACTT CCCCCGTAAA
GCP18-2CP418L-Wes	A. TTGTTT ATACAAGTT .CACT AAAT CTACAAACTT TCCCCGTAAA
GCP18-4CP418L-R2000	A. TTGTTT ATACAAAGTT TCACT AAAT CTACAAACTT TCCCCGTAAA
conse129bal-Drak	A. TTGTTT ATACAAAGTT .CACT AAAT CTACAAACTT TCCCCGTAAA
GCPS18-129Sam-ba2	A. TTGTTT ATACAAAGTT TCACT AAAT CTACAAACTT TCCCCGTAAA
GCP18-3129R211-ba2	AAC.CAGTTTC TTGCAATAGTT TCACTAAAT CTACAAACTT TC.....
GCP18-10129R20-ba2	AACACAGTTTC TTGCAATAGTT TCACT AAAT CTACAAACTT TC.....
Consensus	A.CCCAGTTTC TTGCAATAGTT TC.CT. AAAT CTTACAAACTT TC.....

Figure 15 (b)

EMBH44836anti	TGAGCTTAAT	ATCACCCAA.	GATGTTTCA	ATCAGAT	AAA	GAGTAACGAC
GCP18-5CP418L-Sams	TGAGCTTAAT	ATCACCCAAA	GATGTTTCA	ATCAGAT	AAA	GAGTAACGAC
GCP18-2CP418L-Wes	TGAGCTTAAT	ATCACCCAAA	GATGTTTCA	ATCAGAT	AAA	GAGTAACGAC
GCP18-4CP418L-R2000	TGAGCTTAAT	ATCACCCAAA	GATGTTTCA	ATCAGAT	AAA	GAGTAACGAC
conse129bal-Drak	TGAGCTTAAT	ATCACCCAAA	GATGTTTCA	ATCAGAT	AAA	GAGTAACGAC
GCPS18-129Sam-ba2AT	CTTATCTAAA	G..TTATCAC	ATCACAT	GAA	GA.....
GCPR18-3129R211-ba2AT	CTTATCTAAA	G..TTATCAC	ATCACAT	GAA	GA.....
GCP18-10129R20-ba2AT	CTTATCTAAA	G..TTATCAC	ATCACAT	GAA	GA.....
Consensus
401						
EMBH44836anti	ATCGTTTGA	GATTAGAACAA	AA			
GCP18-5CP418L-Sams	ATCGTTTGA	GATTAGAACAA	AA			
GCP18-2CP418L-Wes	ATCGTTTGA	GATTAGAACAA	AA			
GCP18-4CP418L-R2000	ATCGTTTGA	GATTAGAACAA	AA			
conse129bal-Drak	ATCGTTTGA	GATTAGAACAA	AA			
GCPS18-129Sam-ba2GAGC	AA			
GCPR18-3129R211-ba2GGC	AA			
GCP18-10129R20-ba2GGC	A.			
Consensus			
431						
EMBH44836anti	CTGAAACTTA	CGTAGAGTGA	TTTGAGGAGT	AGGCTCGTTG	CCAGCAGAGC	
GCP18-5CP418L-Sams	CTGAAACTTA	CGTAGAGTGA	TTTGAGGAGT	AGGCTCGTTG	CCAGCAGAGC	
GCP18-2CP418L-Wes	CTGAAACTTA	CGTAGAGTGA	TTTGAGGAGT	AGGCTCGTTG	CCAGCAGAGC	
GCP18-4CP418L-R2000	CTGAAACTTA	CGTAGAGTGA	TTTGAGGAGT	AGGCTCGTTG	CCAGCAGAGC	
conse129bal-Drak	CTGAAACTTA	CGTAGAGTGA	TTTGAGGAGT	AGGCTCGTTG	CCAGCAGAGC	
GCPS18-129Sam-ba2	GTAAACCTTA	CTAGAGTGA	TGTGAGGAGT	AGGCTCGTTG	CCAGC.....GAGC	
GCPR18-3129R211-ba2	GTAAACCTTA	CTAGAGTGA	TGTGAGGAGT	AGGCTCGTTG	CCAGC.....GAGC	
GCP18-10129R20-ba2	GTAAACCTTA	CTAGAGTGA	TGTGAGGAGT	AGGCTCGTTG	CCAGC.....GAGC	
Consensust.tgaggtaggctcgttg	ccagc.....gagc	
480						
EMBH44836anti	TAGCTCTCTC	CTCCGCCCTCA	TGAAGCATTCT	GTTGCACCTG	AGACAACCGT	
GCP18-5CP418L-Sams	TAGCTCTCTC	CTCCGCCCTCA	TGAAGCATTCT	GTTGCACCTG	AGACAACCGT	
GCP18-2CP418L-Wes	TAGCTCTCTC	CTCCGCCCTCA	TGAAGCATTCT	GTTGCACCTG	AGACAACCGT	
GCP18-4CP418L-R2000	TAGCTCTCTC	CTCCGCCCTCA	TGAAGCATTCT	GTTGCACCTG	AGACAACCGT	
conse129bal-Drak	TAGCTCTCTC	CTCCGCCCTCA	TGAAGCATTCT	GTTGCACCTG	AGACAACCGT	
GCPS18-129Sam-ba2	TAGCTCTCTC	CTCCGCCCTCA	TGAAGCATTCT	GTTGCACCTG	AGACAACCGT	
GCPR18-3129R211-ba2	TAGCTCTCTC	CTCCGCCCTCA	TGAAGCATTCT	GTTGCACCTG	AGACAACCGT	
GCP18-10129R20-ba2	TAGCTCTCTC	CTCCGCCCTCA	TGAAGCATTCT	GTTGCACCTG	AGACAACCGT	
Consensus	tagctctctc	ctccgccc	tgaagcattct	9.tgacac	tgacac	tgacac
530						
EMBH44836anti	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCP18-5CP418L-Sams	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCP18-2CP418L-Wes	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCP18-4CP418L-R2000	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
conse129bal-Drak	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCPS18-129Sam-ba2	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCPR18-3129R211-ba2	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCP18-10129R20-ba2	GACGAAACTT	TCCGATCCCC	GCC.CCAGAA	TTCGACGCCG	CGCATCGGAA	
Consensus	gacgaaactt	tccgatcacc	gcccaccagaa	ttcgacccgg	cgcatcgaa	cgcatcgaa
531						
EMBH44836anti	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCP18-5CP418L-Sams	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCP18-2CP418L-Wes	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCP18-4CP418L-R2000	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
conse129bal-Drak	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCPS18-129Sam-ba2	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCPR18-3129R211-ba2	GACGAAACTT	TCCGATCACC	GCCACCAGAA	TTCGACGCCG	CGCATCGGAA	
GCP18-10129R20-ba2	GACGAAACTT	TCCGATCCCC	GCC.CCAGAA	TTCGACGCCG	CGCATCGGAA	
Consensus	gacgaaactt	tccgatcacc	gcccaccagaa	ttcgacccgg	cgcatcgaa	cgcatcgaa
581						
EMBH44836anti	CGATCCGAAT	CGGGAACTGG	AGTGAACCCG	AGCGATCCCC	GGAGTGCAC	
GCP18-5CP418L-Sams	CGATCCGAAT	CGGGAACTGG	AGTGAACCCG	AGCGATCCCC	GGAGTGCAC	
GCP18-2CP418L-Wes	CGATCCGAAT	CGGGAACTGG	AGTGAACCCG	AGCGATCCCC	GGAGTGCAC	
GCP18-4CP418L-R2000	CGATCCGAAT	CGGGAACTGG	AGTGAACCCG	AGCGATCCCC	GGAGTGCAC	
conse129bal-Drak	CGATCCGAAT	CGGGAACTGG	AGTGAACCCG	AGCGATCCCC	GGAGTGCAC	
GCPS18-129Sam-ba2	CGATCCGAAT	CGGGAACTGG	AGTGAACCCG	AGCGATCCCC	GGAGTGCAC	
GCPR18-3129R211-ba2	CGATCCGAAT	CGGGAACTGG	AGTGAACCCG	AGCGATCCCC	GGAGTGCAC	
GCP18-10129R20-ba2	CGATCCGAAT	CGGGAACTGG	AGTGAACCCG	AGCGATCCCC	GGAGTGCAC	
Consensus	ggatccgaat	cgggaaactgg	agtgaacc.g	agcgatcccc	ggagtgcac	ggagtgcac
630						

Figure 15 (c)

631	EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCP18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG ggagcg.tgg .aaaagagag tggcacgatt tcgacgaaga g.ggaagagg	690
691	EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCP18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCTCA TCGTCCCTGAT AGAGGGTGGT ggataaaactc gcgtatgatc aagttctca tcgtccctga.	740
741	EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak GCP18-129Sam-ba2 GCPR18-3129R211-ba2 GCP18-10129R20-ba2 Consensus	TGCCGCCATT TTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG TGCCGCCATT TTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG TGCCGCCATT TTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG TGCCGCCATT TTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG TGCCGCCATT TTTTTGTCA GGGCGCTCTG .GGCTTAGAA GTTTCCGATG TGCCGCCATT CTTGTTCAC. .GGCGCTCTG GGT..... TGCCGCC. TGCC..CAT. CTTGAGCTC. .GG.GCGCGG GCTCACAA. tgccgccat. .tt.....c. .gg.gc.c.g	pSG129antiu 790
791	EMBH44836anti GCP18-5CP418L-Sams GCP18-2CP418L-Wes GCP18-4CP418L-R2000 conse129bal-Drak	TCAATGAAC A GTGACACGAC GAAATGC TCAATGAAAC AGAAT...TC CGGG... CCAATGAACA AGATTATTC CGATG..	800

Figure 16

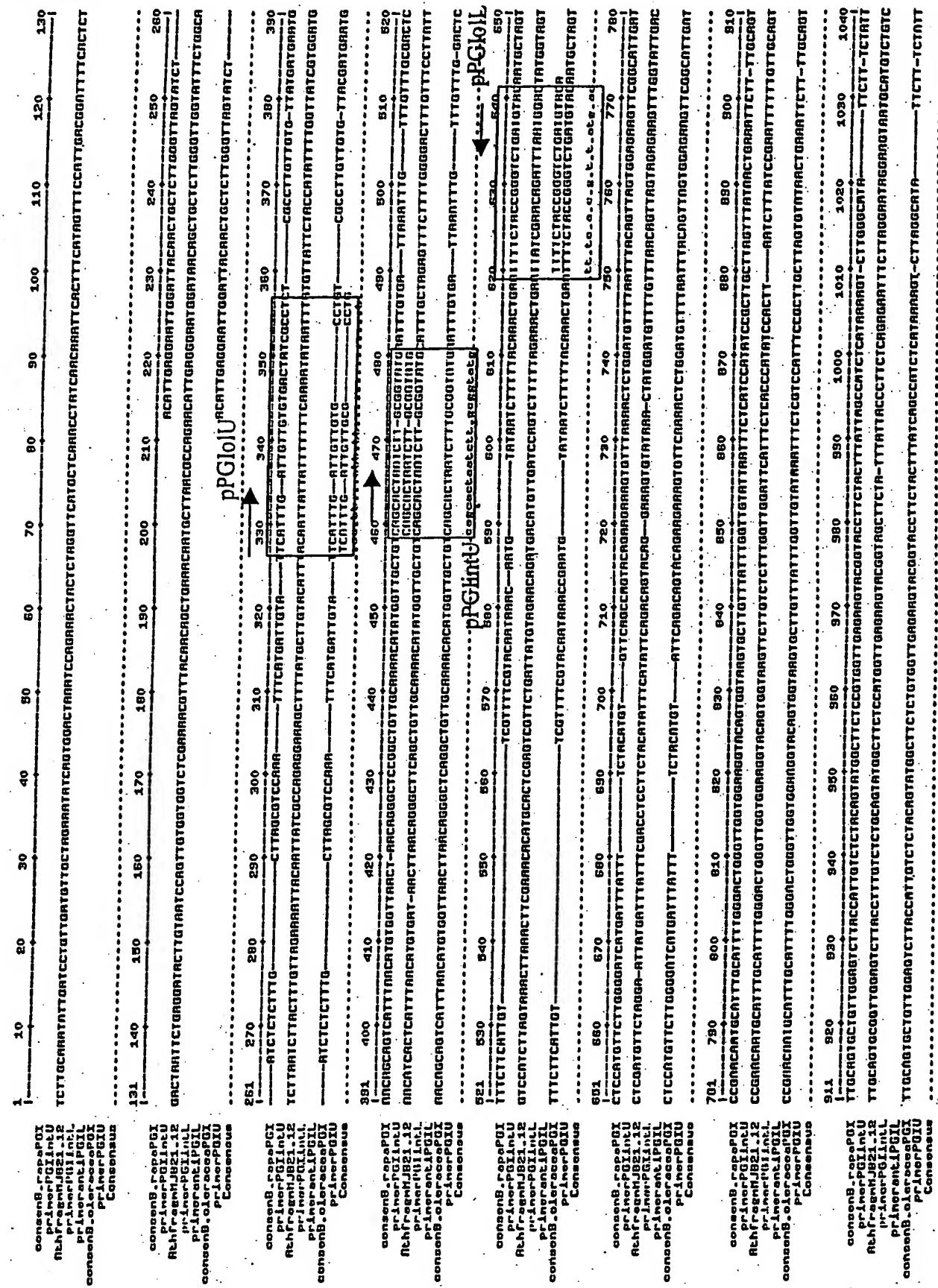


Figure 16 BIS

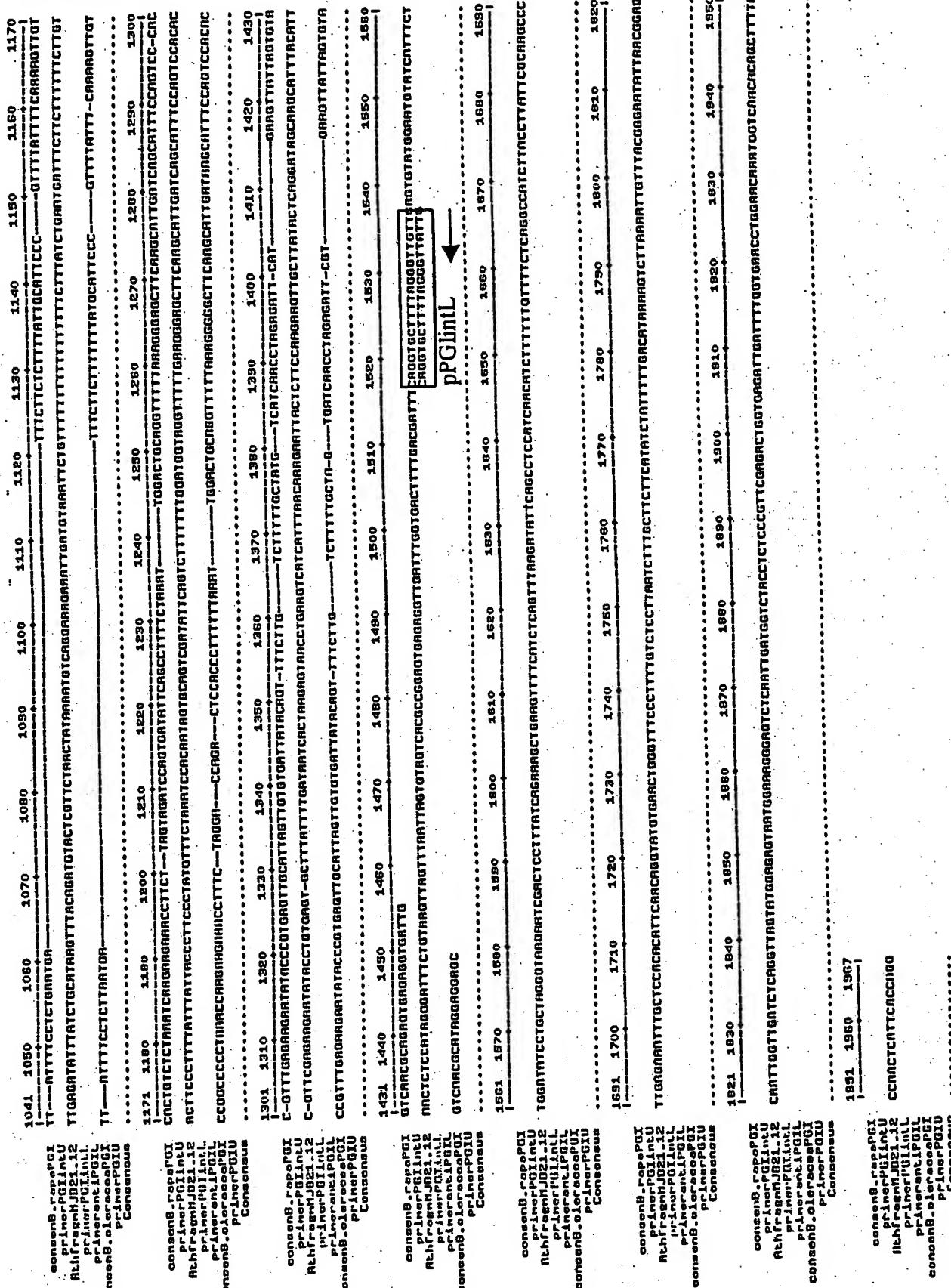


Figure 17

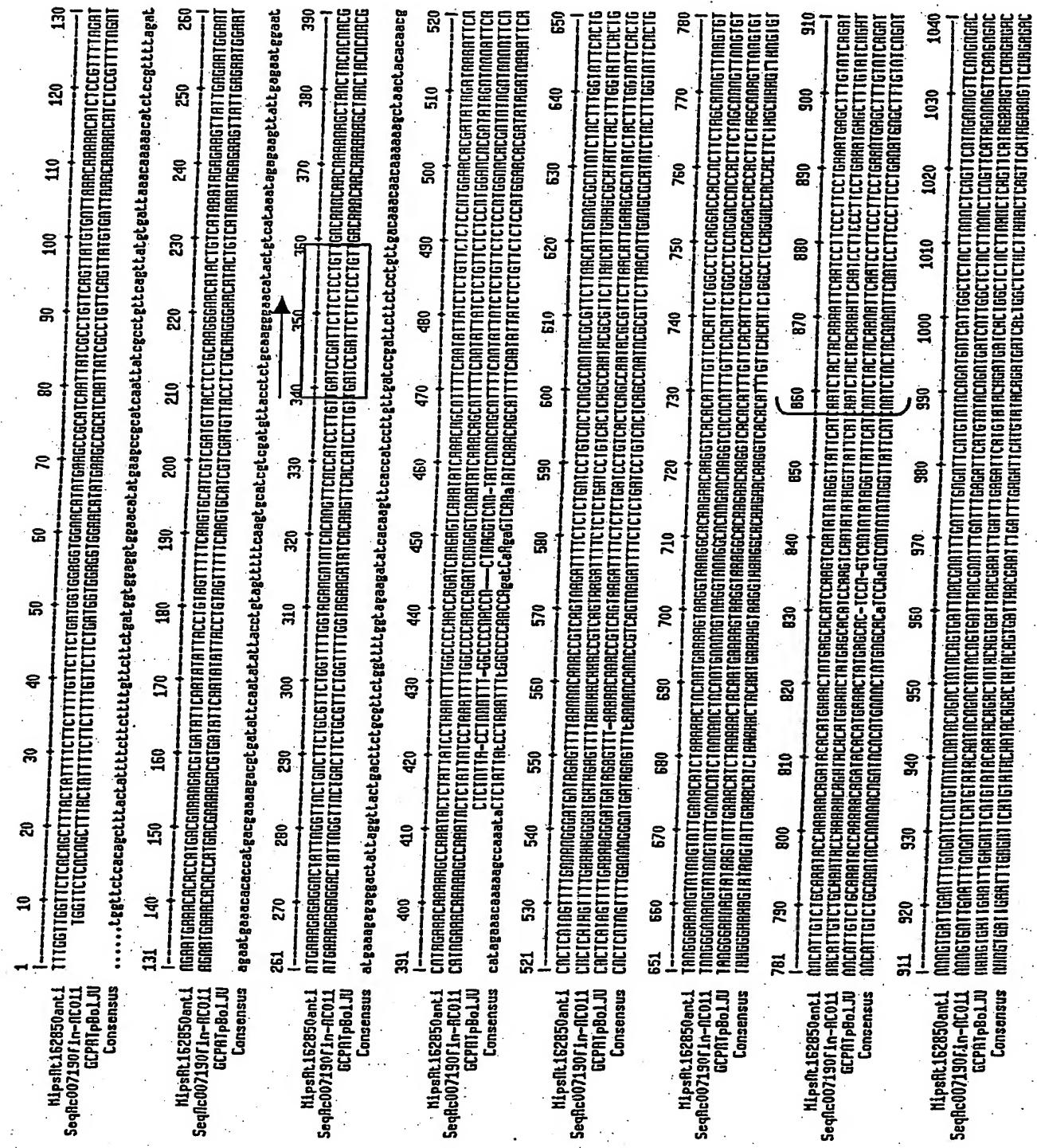
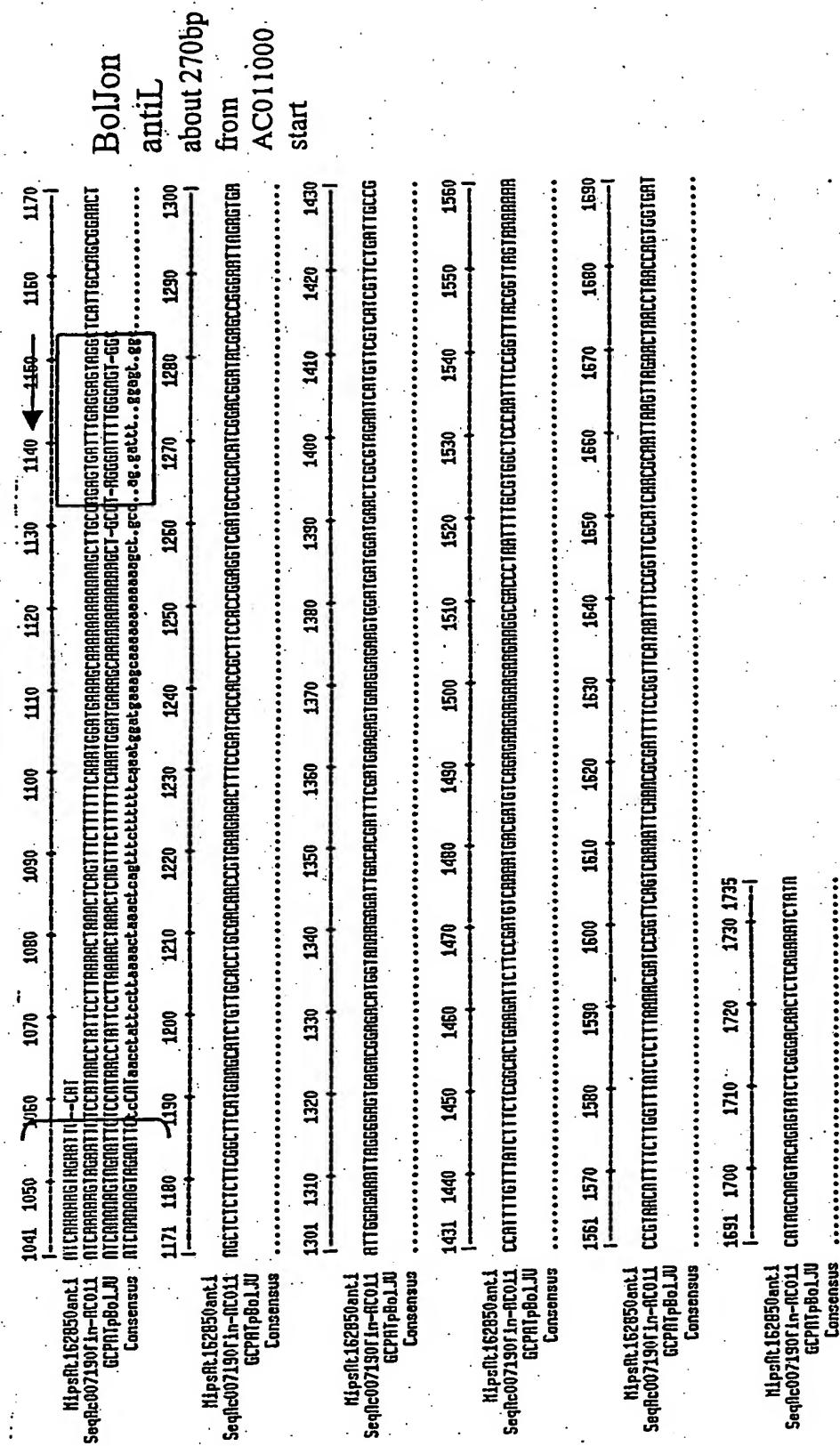


Figure 17 BIS



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